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(54) Title: HUMAN LACTOFERRIN

(57) Abstract

The present invention relates to a human lactoferrin cDNA gene obtained from human breast tissue and the protein encoded therefrom. The present invention further relates to methods for detecting malignancy arising from tissues that normally secrete lactoferrin using the cDNA gene probe of the present invention. Another aspect of the present invention relates to the promotor region that regulates the human lactoferrin gene.

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HUMAN LACTOFERRIN

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

The present invention relates to a human lactoferrin gene isolated from breast tissue and to the protein product encoded therein. The present invention further relates to the promotor region of human lactoferrin gene and to methods for detecting and analyzing malignancies arising from tissues that normally secrete lactoferrin using a novel human lactoferrin cDNA gene sequence.

BACKGROUND INFORMATION

Lactoferrin is a single polypeptide molecule (M_r 76,000) with sites where two oligosaccharide chains can attach (B.F. Anderson et al., *J. Mol. Biol.* 209:711-734 (1989)). This protein shares significant homology with transferrin, however, its role in iron transport is limited since it binds iron 260 times stronger than transferrin (B.F. Anderson et al., (1989)). Two and possibly three isoforms of lactoferrin have been isolated using an affinity chromatography (P. Furnamski et al., *J. Exp. Med.* 170:415-429 (1989); A. Kijlstra et al., *Current Eye Res.,* 8:581-588 (1989)). Lactoferrin has been shown to inhibit bacterial growth by chelating iron and directly attacking the cell wall (R.T. Ellison et al., *Infect Immun.,* 56:2774-2781 (1988)), contribute to the anemia of chronic disease (Birgens. *Scand. J. Haematol.,* 33:225-230 (1984)), improve intestinal absorption of iron in infants (Birgens., (1984)) inhibit myelopoiesis (H.E. Broxmeyer et al., *Blood Cells*

13:31-48 (1987)), and degrade mRNA (P. Furmanski et al., (1989); M.R. Das et al., *Nature* 262:802-805 (1976); P. Furmanski and Z.P. Li, *Exp. Hematol* 18:932-935 (1990). Large quantities of lactoferrin are found in breast milk (B. Lonnerdal et al., *Nutrition Report Int.*, 13:125-134 (1976)), in estrogen-stimulated uterine epithelium (B.T. Pentecost and C.T. Teng, *J. Biol. Chem.* 262:10134-10139 (1987)), and in neutrophilic granulocytes (P.L. Masson et al., *J. Exp. Med.*, 130:643-658 (1969)) with smaller amounts in tears, saliva, serum, and seminal fluid (D.Y. Mason and C.R. Taylor, *J. Clin. Path.*, 31:316-327 (1978)).

While normal breast ductal epithelium and neutrophilic granulocytes contain lactoferrin, their malignant counterparts frequently do not (C. Charpin et al., *Cancer*, 55:2612-2617 (1985); T.A. Rado et al., *Blood*, 70:989-993 (1987)). This has been evaluated at the protein level and in a few samples at the messenger RNA level (T.A. Rado et al., (1987)). Analysis at the genomic level has not been performed. DNA variations, that are detected in the coding regions, may lead to abnormal protein structure and loss of normal function. Variations, such as mutations, deletions, or changes in methylation, at the promoter regions could lead to altered regulation of the gene. Evaluation of the lactoferrin gene may provide interesting insight concerning the production of lactoferrin in malignant cells. Thus, the need exists for the structure of the lactoferrin gene including the cDNA and the promotor region. The present invention provides such a description of the structure of a

human lactoferrin cDNA and promotor region of the gene.

Using a lactoferrin cDNA clone isolated from human breast tissue, the applicants have evaluated restriction fragment length changes in DNA from the white blood cells of 10 normal controls, acute non-lymphocyte leukemia (ANLL) cells from 7 patients, T-cell acute lymphocyte leukemia (ALL) from one patient, 3 leukemia cell lines, and 7 breast cancer cell lines. A comparative study of the lactoferrin gene in these different cell types is provided herein.

The present invention further relates, in part, to a human lactoferrin cDNA and the protein product encoded therein. In another aspect, the present invention relates to methods for detecting malignancy in tissues that normally secrete lactoferrin by evaluating restriction patterns in DNA using a lactoferrin gene probe of the present invention.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a DNA sequence of the human lactoferrin gene including the cDNA and the promotor region and to the protein product encoded therein.

In one embodiment, the present invention relates to a DNA segment encoding human lactoferrin according to the sequence identification number In another embodiment, the present invention relates to the human lactoferrin protein encoded by the sequences given in identification number 2.

In yet another embodiment, the present invention relates to a DNA segment of the promotor region for human lactoferrin according to the sequence identification number 5 and allelic variations thereof.

In a further embodiment, the present invention relates to a recombinant DNA construct comprising the DNA segments encoding the human lactoferrin gene sequences described above and a vector.

In another embodiment, the present invention relates to a recombinant DNA construct comprising the DNA segment encoding the human lactoferrin gene described above and a DNA promotor regulatory region for human lactoferrin according to sequence identification number 5 or portion thereof operatively linked to the DNA fragment.

In a further embodiment, the present invention relates to a host cell comprising the above described constructs.

Another embodiment of the present invention relates to a method of treating a condition in a patient characterized by a deficiency in lactoferrin by administering to the patient an amount of human lactoferrin according to the present invention in sufficient quantities to eliminate the deficiency. The conditions include neutropenia, AIDS, skin infection, gastrointestinal bacterial overgrowth syndrome, vaginal infection and septic shock.

In yet another embodiment, the present invention relates to methods of diagnosing malignancy or detecting the recovery of a malignancy

from a biological sample comprising the steps of isolating DNA from the biological sample and from normal control samples, cutting the DNA with a restriction enzyme called Xba I, hybridizing the cut DNA with a DNA segment of the human lactoferrin gene of the present invention described above or portion thereof under conditions such that hybridization is effected and comparing the hybridization product patterns of the biological sample and the normal control sample with each other.

In a further embodiment, the present invention relates to a method for detecting small insertions, deletions or mutations surrounding the human lactoferrin gene comprising the steps of isolating the DNA from a biological sample suspected of having such an insertion, deletion or mutation, amplifying the DNA using the human lactoferrin gene segment of the present invention described above or portion thereof in a polymerase chain reaction followed by enzymatically cutting the amplified DNA with Xba I, and hybridizing this DNA with the human lactoferrin gene segment described above under conditions such that hybridization is effected and sequencing the hybridized DNA.

Various other objects and advantages of the present invention will become obvious from the drawings and detailed description of the invention.

The entire contents of all publications mentioned herein are hereby incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the immunocytochemical staining of normal bone marrow (A) x 400, and breast cancer cell line SKB R3 (B) x 680 using anti-lactoferrin antibody at 1:1500.

Figure 2 depicts the restriction fragments produced with DNA from normal cells (A) or from leukemia cells (B) using lactoferrin cDNA (HLF 1212) as the probe. Normal samples (n=9) and DNA from 10 different leukemia cells types were digested with indicated enzyme, run in one gel and representative lanes cut out for comparison.

Figure 3 depicts the restriction fragments produced using DNA from normal samples (A) and from breast cancer cell lines (B), using lactoferrin cDNA (HLF 1212) as a probe. Normal samples (n=2) and DNA from eight cancer lines were digested with indicated enzyme, run in the same gel, and representative lanes cut out for comparison.

Figure 4 shows the restriction fragments produced using Msp I and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 - 9 are DNA from normal donors. Lanes 10 - 16 represent DNA from leukemia cells from patients. Lane 17 is cell line K562, lane 18 is KG 1, and lane 19 is U937.

Figure 5 represents the restriction fragments produced using Msp I and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 and 2 are DNA from normal donors. Lanes 3 - 9 represent DNA from breast

cancer cell lines. The cell lines are in the following order: Lane 3 - MDAMB 468, lane 4 - MCF 7, lane 5 - BT 474, lane 6 - HBL 100, lane 7 - MDA 175, lane 8 - SKB R3, lane 9 - ZR 75-1.

Figure 6 shows the restriction fragments produced using Xba I and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 - 9 are DNA from normal donors. Lanes 10 - 16 are DNA from leukemia cells from patients and lanes 17 - 19 DNA from leukemia cell lines (lane 17 - K562, lane 18 - KG1, lane 19 - U937). Arrow A is the band found is patterns A (lanes 1, 2, and 7), B, and C. Arrow B is the band found in patterns B (lanes 3 - 6, 8 - 10, 13, 14) and C. Arrow C is only found in pattern C (lanes 11, 12, 16). Insert is the same specimens run on a 0.7% agarose gel.

Figure 7 depicts the restriction fragments produced using Xba I and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 and 2 are DNA from normal donors. Lanes 3 - 9 are DNA from breast cancer cell lines. The order is: Lane 3 - MDAMB 468, lane 4 - BT 474, lane 5 - HBL 100, lane 6 -MDA 175, lane 7 - SKB R3, lane 8 - ZR 75-1, lane 9 - ZR 75-30. Restriction fragment patterns as discussed in the text are in the following lanes: pattern A is seen in lane 1, pattern B in lane 2, and pattern D in lanes 3 - 9.

Figure 8 shows the restriction fragments produced using Hpa II and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 - 9 are DNA from normal donors. Lanes 10 - 16 are DNA from leukemia cells from

patients. Lane 17 is cell line KG1, lane 18 is U937, and lane 19 is HL 60.

Figure 9 shows the restriction fragments produced using Hpa II and lactoferrin cDNA (HLF 1212) as the probe. Lanes 1 and 2 are DNA from normal donors. Lanes 3 - 10 are breast cancer cell lines in the following order: lane 3 - MDAMB 468, lane 4 - MCF 7, lane 5 - BT 474, lane 6 - HBL 100, lane 7 - MDA 175, lane 8 - SKB R3, lane 9 - ZR 75-1, lane 10 - ZR 75-30.

Figure 10 depicts a sequence data of HLF 1212. Differences between the published protein derived AA sequence and our cDNA derived sequence are indicated by underlining the extra AA in our sequence or indicating substitutions beneath our sequence. Nucleotide differences based on published sequence data are indicated above our sequence. Nucleotide changes resulting in a different AA are typed below the area of substitution.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a cDNA sequence for human lactoferrin and the protein encoded therein. The cDNA called HLF1212 was isolated from human breast tissue and is 2117 kb in length. The sequence agrees with the modified amino acid sequence of iron-binding lactoferrin in all areas except the 3 sites in the N-terminal region. One further change is in arginine in place of a lysine at amino acid 200.

Another aspect of the present invention relates to methods for diagnosing malignancy by

restriction fragment length polymorphisim (RFLP) analysis of DNA extracted from normal peripheral blood and leukemia cells from patients using the cDNA of the present invention as the probe. Southern analysis indicates that the human lactoferrin gene is polymorphic when tested using Msp I and Xba I restriction enzymes. Further analysis indicates that the changes in the XbaI recognition site could be explained by alterations in DNA caused by or resulting in malignancy. In the present invention, the DNA from normal and malignant cells are digested with XbaI and the fragment pattern compared using methods well known in the art. The Xba I restriction is associated with 4 patterns in normal and malignant cells (Example 3 and Figures 6 and 7). The most striking change is the deletion of many bands found only in DNA obtained from malignant cells or cell lines derived from either leukemia or breast cancer.

If the patterns found in Example 3 (Xba I RFLP pattern C + D) are found in women before breast cancer occurs, it may be easy to screen women at high risk of breast cancer for these changes using cDNA probe of the present invention and RFLP methodologies well known in the art. For example, lymphocytes may be separated from peripheral blood, DNA extracted, and cut with XbaI. This DNA can then be probed with HLF 1212 or a small piece of HLF 1212 and patterns determined. High risk patients may be placed on preventive medicines such as Tamoxifen retinoids or have surgery. The same may hold for other hormonally responsive tumors such as prostrate, uterus, or tumors arising from

lactoferrin secreting organs such as leukemia, or salivary gland.

Another aspect of the present invention relates to RFLP methods to measure the prognosis of certain types of cancer patients that are given therapeutics. One may place patients with breast, prostrate, uterine, or salivary cancer into risk groups. Those with a specific pattern may be at different risks of disease reoccurence. Thus, RFLP analysis using the cDNA probe of the present invention may provide prognostic information for patients with cancer.

Another aspect of the present invention relates to methods for detecting small insertions, deletions or mutations surrounding the human lactoferrin gene. Either of the above described RFLP methods could be combine with polymerase chain reaction (PCR) analysis. The abnormal area of the gene may be amplified using methods well known in the art and then mutations detected using restriction analysis (i.e. Xba I) and sequencing.

Yet another aspect of the present invention relates to methods for detecting tumors in pathological specimens that may contain too few malignant cells to be detected by standard methods. This method may involve PCR of DNA extracted from specimens (biopsy of tissue or bone marrow) and subsequent analysis using the RFLP techniques and DNA probes described above and in the Examples.

In another embodiment, the present invention relates to the cDNA clone for human lactoferrin called HLF 1213 and the protein encoded therein. The sequence of HLF 1213 (sequence ID

NO:3) is a combination of clones HLF 1212 (sequence ID NO: 1), 031A (sequence ID NO: 5) and other clones isolated in the same method as HLF 1212. (See Example 2). This clone is a composite of the complete human lactoferrin cDNA. This clone may be constructed by splicing 2 clones together with HLF 1212 (031A, and HLF 1212). Both HLF 1212 or this combined fragment called HLF 1213 may be used to make recombinant human lactoferrin.

In another embodiment, the present invention relates to the human lactoferrin protein obtained from HLF 1212 and HLF 1213 called sequence ID Numbers 2 and 4 respectively.

In yet another embodiment, the present invention relates to recombinant human lactoferrin expressed in vitro through molecular genetic engineering technology.

The present invention also relates to the recombinant DNA molecules and to host cells transformed therewith. Using standard methodology well known in the art and described briefly below, a recombinant DNA molecule comprising a vector, for example, a Bacculovirus transfer vector and a DNA fragment encoding human lactoferrin, for example, HLF 1212 or 1213, can be constructed without undue experimentation.

The methods of choice is the Baculovirus-insect cell expression system (M.D. Summers and G.E. Smith, *Texas Agriculture Experiment Station Bulletin* No. 1555, (1987); V.A. Luckow et al., *Bio/technology* 6:47-55 (1988)). This system has been used successfully to produce commercial quantities of recombinant mammalian glycoproteins. Other expression systems known in

the art can also be used to produce the recombinant protein, for example, yeast, bacterial or mammalian cells.

The 2.2 Kb Eco-R1 fragment containing the entire human lactoferrin coding region may be removed from plasmid HLF 1212 or HLF 1213. The lactoferrin cDNA may be subcloned into Baculovirus transfer vector pAc 700 series (T. Maniatis et al., *Molecular Cloning*: a laboratory manual, Cold Spring Harbor Laboratories, Cold Spring Harbor, New York). Recombinant plasmid (Achlf) may be co-transfected into Sf9 cells along with wild-type AcNPV viral DNA by calcium phosphate transfection procedure (M.D. Summus and G.E. Smith). <u>In vivo</u> homologous recombination between the polyhedron sequences in the wild type viral DNA and the recombinant plasmid results in the generation of recombinatn viruses coding for a fused gene product. The recombinant viruses may be plaque purified by screening for the occlusion negative (polyhderon negative) phenotype or by colony hybridization using ^{32}P-DNA probes covering the HLF-coding region. Characterization of the recombinant viral DNA may be carried out as described by Maniatis et al. Sf9 cells may be plated in 24-well dishes (Costar) at 3×10^5 cells/well and allowed to attach for 2 hours in complete Graces medium. Cells are then infected with wild type AcNPV or recombinant virus AchLF. Two days post-infection, the cell layer and the condition medium may be collected and assayed for the presence of hLF. HLF can be analyzed by SDA-PAGE and Western blotting. Iron binding capacity and anti-bacterial acitivity may also be examined.

The present invention further relates to treatment of antibacterial and antiviral infections using pharmaceutical doses of human lactoferrin of the present invention (HLF 1212 and 1213 corresponding to sequence ID Nos. 2 and 4 respectively) or recombinant human lactoferrin protein of the present invention.

The actions of lactoferrin are varied; the best established function is antibacterial (R.R. Arnold et al., *Science* 197:263-265 (1977)). Patients have been found whose neutrophils are deficient in lactoferrin (K.J. Lomax et al., *J. Clin. Invest.* 83:514-519 (1989)). These patients are prone to recurrent infections. Lactoferrin also has been found to decrease release of CSF or monokines, enhancement monocyte natural killer activity, enhancement of hydroxyl radical production and modulate the activation of the complement system (Birgens, *Scand. J. Haematol* 33:225-230 (1984)). There is also early <u>in vivo</u> evidence of lactoferrin antiviral activity.

In the past few years, HIV infection has become a significant health problem. HIV causes morbidity by crippling the body's defense mechanism and allowing development of opportunistic infections. Present treatment is less than ideal and involves treating opportunistic infections as they occur or inhibiting reverse transcriptase. Human lactoferrin is the natural product of the human defense machinery and has been given to patients both orally and intravenously with no side effects. Due to its bacteriocidal, antifungal, and immunoregulatory activity, administering pharmaceutical acceptable doses of lactoferrin of

the present invention could prove an effective agent to treat patients with AIDS or patients with neutropenia.

Other possible uses of the human lactoferrin of the present invention include treatment of lactoferrin in pharmaceutical doses, either orally or intravenously to patients with skin infections (burn patients), gastrointestinal bacterial overgrowth syndromes, vaginal infections, septic shock, and numerous other disorders.

In yet another embodiment, the present invention relates to the genomic human lactoferrin promotor region (sequence ID No: 5). This sequence contains the entire human lactoferrin promotor region fragment including exon 1 of human lactoferrin clone 1212.

The 5' genomic regulatory region of the present invention has the ability to regulate DNA in a tissue specific manner, i.e., it can be on in breast tissue and off in skin. It also can be hormonally regulated, i.e., on in mid-cycle menstrual cycle, off at menses. This regulation ability may be used in several ways. Genes targeted for transgenic mice may use the lactoferrin promotor. Genes to be used in therapy of human disease (gene therapy) may be linked to the lactoferrin promotor and thus the therapeutic gene regulated in a tissue specific or hormonal pattern.

The invention is described in further detail in the following non-limited examples.

EXAMPLES

The following procedures and materials were used througout the Examples.

Human tissue.

150 ml of heparinized blood or 5 ml heparinized bone marrow was obtained from normal paid donors after informed consent was obtained. Informed consent and leukemia cells were obtained from seven patients with acute leukemia undergoing emergent leukapheresis. The FAB classification of the patients were: two patients with M2, two patients with M7, and one patient each with M4, M7, ANLL not further specified, and T-cell ALL. Nucleated cells were obtained from 80 ml of blood from normal donors after first incubating cells at 37° C for 30 min. in 1:20 diluted methylcellulose (30 g/500 ml Hank balanced salt solution (HBSS) to sediment the red blood cells. The leukocyte-rich fraction was removed, and centrifuged into a pellet at 500 x g for 10 min. at 4° C. Cells from patients with leukemia were either used fresh or diluted in RPMI 1640 containing 20% fetal calf serum and 10% dimethylsulfoxide (DMSO), then frozen at -70° C until use. Human leukocyte antigen (HLA) typing, cytogenetic analysis, and bone marrow biopsy results were available for all but one patient who died shortly after leukapheresis. All cell lines were originally obtained from ATCC (Rockville, MD) and maintained at 37° C, 93% humidity, and 5% CO_2. Breast cancer cell lines and HBL 100 (a cell line derived from a lactating breast) were maintained and provided by Dr. J. Dirk Iglehart (Department of

Surgery, Duke University). Cells were grown to confluence and separated from dishes with trypsin 0.05%/EDTA (Gibco), washed, and centrifuged. For all samples, DNA was isolated according to standard methodology (W.M. Strauss in Current Protocols in Molecular Biology. F.A. Ausebel, et al., (eds.), pp. 2.2.1 - 2.2.3 1990. Greene Publishing and Wiley-Interscience, New York.

Isolation of cDNA

A Clonetech cDNA library from normal human breast tissue (HL 1037b) was plated in host cells Y1090, filter-lifted and probed with mouse lactoferrin cDNA T267 (B.T. Pentecost and C.T. Teng, (1987)). Positive clones were plaque-purified, and the inserts subcloned into the Eco R1 site of Bluescript II SK+ (Stratagene). The recombinant clones were transformed into XL1 Blue cells (Stratagene). A 2.1 Kb insert (HLF 1212) was isolated and sequenced using the dideoxy nucleotide termination reaction and [^{35}S]dATP label under contract by Lark sequencing company.

Southern Analysis

Ten μg of DNA was digested at 37° C for three hours with Eco R1, Bam H1, Hind III, Pvu II, Pst I, Msp I, Xba I, Hpa II, Mbo I or Sau 3AI under conditions specified by the manufacturer (BRL). Hpa II and Sau 3AI will not cleave DNA when specific bases within their recognition sites are methylated. Msp I and Mbo I respectively, recognize these same sites and are methylation insensitive. DNA was loaded into 0.7, 0.8, or 1.2% agarose gels, run

overnight, and transferred either to Genescreen Plus (nylon, DuPont) or BA-S NC (nitrocellulose, Schleicher & Schuel). Lactoferrin cDNA was removed from plasmid with Eco RI, redigested with Pst I, and gel purified. Both fragments were labeled with [^{32}P]dCTP using a random primer kit (Stratagene) to a specific activity of 1 x 10^9. Hybridization was performed exactly according to Genescreen instructions or a modification of BA-S NC instructions (hybridization solution - 50% formamide, 5x SSPE, 1% SDS, 4x Denhardt, 100 μg/ml single stranded DNA, 7.5% dextran, pre-hybridization solution - the same as above with 5% formamide and no dextran). Filters were washed at high stringency at 60° C and exposed to Kodak XOMAT AR film using intensifying screens for 3-7 days. DNA from normal and leukemic cells was probed with histone cDNA (Oncore) as a control; no polymorphic pattern was found.

Immunocytochemistry

Antibody against human milk lactoferrin (Sigma) was raised in rabbits and the IgG fraction was prepared as described previously (C.T. Teng et al., *Endocrinology* 124:992-999 (1989)). All cell lines, normal cells, and leukemia patient's cells were examined using this antibody. Ten normal bone marrow specimens were stained to define the specific cell in bone marrow that begins to produce lactoferrin. Cells were smeared onto alcohol-washed, pre-cleaned slides, air dried 1 hour, and fixed in 95% methanol, and 1.7% formalin for 10 min. Slides were next rinsed in dH_2O and either air dried and stored in a moisture proof container at 4° C or

used immediately. Staining procedure was followed directions provided with Vector ABC-AP kit using levamisol as the blocking agent, antibody dilution of 1:1500, and hematoxylin (gill #3) counterstain. Three-hundred cells per sample were scored manually as negative, trace, or positive.

Example 1. Immunocytochemical staining.

As shown in Table 1 and Figure 1A, bone marrow lactoferrin began to appear in the myelocyte stage with almost all cells staining positively by the metamyelocyte stage. None of the leukemia cells from patients or leukemia cell lines contained stainable lactoferrin. Occasional positive granulocytes could be seen in with the leukemic cells from patients. Breast cancer cell lines stained negatively for lactoferrin except for 1.5% trace positive cells in SKB R3 (Figure 1B).

Table 1. Immunocytochemical staining of normal bone marrow using anti-lactoferrin antibody

	Blasts and Promyelocytes	Myelocytes	Metamyelocytes	Bands	Neutrophils
Negative	93%[α] (8.6)	30% (20.4)	12% (7.5)	3% (1.2)	1% (1)
Trace	6% (8.2)	38% (8.3)	40% (10.6)	10% (5.2)	2% (2)
Positive	0.3% (0.4)	32% (19.2)	48% (17)	88% (4.5)	97% (2)

α - values represent the mean of 10 bone marrow samples stained with the standard deviation in parenthesis, >300 cells counted per sample.

<u>Example 2</u>. Library screening, isolation and characterization of HLF 1212 clone.

Thirty human lactoferrin clones were isolated from the breast tissue cDNA library. The longest (HLF 1212) was sequenced completely. This clone is 2117 bp's in length and includes a 17 amino acid (AA) leader sequence (no ATG site) and is 4 AA shy of the 3' terminus (Figure 10). The AA sequence coded for by HLF 1212 has 4 sites that differ from the previously published revised AA sequence derived from the protein (B.F. Anderson et al., (1989)). In the sequence of the present invention, there is one insertion (Arginine (Arg) at AA 22, bp 64-6) and three substitutions (Glutamine (Gln) for Asparagine (Asn) at AA 31, bp 91-3; Isoleucine (Ile) for Leucine (Leu) at AA 55, bp 163-5; and Arg for Lysine (Lys) at AA 218, bp 652-4). The first three of these changes are clustered at the 5' end. Contained within HLF 1212, but not in any of the 10 other partially sequenced isolates, is a deleted cytosine at bp 2097 (AA 699) which caused a frame-shift at the 3' end of the protein. This extra base was confirmed by repeated bi-directional sequencing. The deletion at 2097 is now thought to be either a cloning artifact or a rare species of mRNA.

In addition to cDNA of the present invention, three other authors have published lactoferrin cDNA sequence data (T.A. Rado, et al., (1987); M.J. Powell and J.E. Ogden, *Nucleic Acids Res.*, 18:4013, (1990); M.W. Rey et al., *Nucelic Acids Res.*, 18:5288, (1990)). All of these sequences are different, and a comparison between the AA data derived from the protein and sequence changes derived from the cDNA, are presented in Figure 10. When compared to HLF 1212, all of the sequences

contain an extra cytosine at bp 2097 (AA 699). Powell et al., (1990) isolated a 2.3 kb sequence from breast tissue that, except for the extra cytosine, is identical to our cDNA in the areas of overlap. The isolate of the present invention differs from that of Rado's 3' 1023 base fragment in 4 locations (T.A. Rado et al., (1987)) with one resulting difference in the AA sequence (Gly for Ala at AA 486, bp 1456-8). Two silent mutations and the extra cytosine make up the remainder of the changes. Ray et al have also published a cDNA sequence isolated from human mammary tissue that contains two AA changes (Ile for Thr at AA 147, bp 440-2; and Gly for Cys at AA 421, bp 1261-3) and one silent base difference (M.W. Rey et al., (1990)).

Example 3. Evaluation of restriction fragments using lactoferrin HLF 1212 as probe.

The fragments produced by digestion with Eco RI, Bam HI, Hind III, Pst I, Pvu II, Sau 3AI, or Mbo I, were nearly identical whether the DNA was from normal or malignant cells. The fragment patterns produced by these restriction enzymes in DNA from leukemic and breast cancer cells are shown in Figures 2 and 3. Restriction with Msp I indicated the deletion of a 3.5 Kb band in 3 of 10 leukemic cells (Figure 4), 4 of 7 breast cancer cell lines (Figure 5), and a much fainter hybridization of this band in 2 of 9 normal specimens (Figure 4). An extra 1.3 Kb band also occurred in the breast cancer line MDA 175 (Figure 5, lane 7). There was no relationship between the phenotype or chromosome

analysis of the leukemia patients and the Msp I changes.

Fragments produced by Xba I fell into 4 patterns. All patterns contained 4 unchanged bands (~6.5 kb, ~4.2 kb, ~3.0 kb, and ~2.2 kb). Pattern A occurred in 3 of 9 normal samples and contained a 3.5 Kb band and three light < 2.0 kb bands in addition to the unchanged bands (Figure 6, lanes 1, 2, and 7; Figure 7, lane 1). Pattern B was seen in 6 of 9 normal and 3 of 7 leukemia cells from patients and contained extra 3.5, 5.0, and 6.7 Kb bands along with the three light < 2.0 kb bands and the unchanged bands (Figure 6, lanes 3-6, 8, 9, 10, 13, 14; Figure 7, lane 2). The last patterns were only seen in DNA obtained from malignant tissue. In pattern C, an extra 9.0 Kb band together with the 3.5, 5.0, and 6.6 kb and unchanged bands were observed in three leukemia patient samples (Figure 6 lanes 11, 12 (see insert) and lane 16). Also noted is the absence of the light < 2.0 kb bands. Pattern D contained only the 4 unchanged and the three light < 2.0 kb bands and was present in DNA obtained from all three leukemia and all seven breast cancer cell lines, (Figure 6, lanes 17 - 19, and Figure 7, lanes 3 - 9). There was one patient (M2 leukemia) with a restriction pattern like that of the cell lines (Figure 6, lane 15). There were no chromosomal abnormalities, French-American-British (FAB) categories, or phenotypic types associated with any polymorphic Xba I pattern.

Example 4. Isolation and characterization of the genomic lactoferrin promotor region.

A human placental DNA library (Clontech) was plated on LE 392 bacterial cells and screened and probed with the 5' end of HLF 1212 (1.3Kb). Positive clones were cut with SAC 1 and rescreened using a 25 base oligonucleotide (synthesized to match Exon 1 of p1212). All SAC 1 fragments from clone 031A were transformed into Bluescript II KS (stratagene) plasmid. Clone 031A-30 was 2.0 kb and hyridized to Exon 1 oligonucleotide probe. This was sequenced using dideoxynucleotide chain termination and synthesized oligonucleotide primers. Sequence ID NO. 5 shows the sequence of the entire fragment (5' - 3') that includes Exon 1.

* * * *

While the foregoing invention has been described in some detail for purpose of clarity and inderstanding, it will be clear to one skilled in the art from a reading of this diclocure that various changnes in form and detail can be made without departing from the true scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Teng, Christina
Panella, Timothy J.

(ii) TITLE OF INVENTION: HUMAN LACTOFERRIN

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
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(E) COUNTRY: USA
(F) ZIP: 20036-5601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SCOTT, WATSON T.
(B) REGISTRATION NUMBER: 26,581
(C) REFERENCE/DOCKET NUMBER: WTS/5683/84482/KIK

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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  1               5                  10                  15

GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC CAA CCC      96
Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln Pro
             20                  25                  30

GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG CGT     144
Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg
         35                  40                  45

GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG TGT ATC     192
Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
     50                  55                  60

CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT GGT GGT     240
Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
 65                  70                  75                  80

TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT GTA GCG     288
Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
                 85                  90                  95

GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT GCC     336
Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
            100                 105                 110

GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA CTG CAA     384
Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
        115                 120                 125

GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA TGG AAT     432
Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
    130                 135                 140

GTC CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT CCA CCT     480
Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
145                 150                 155                 160
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GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC TGT GTT      528
Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
                165                 170                 175

CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT GCG      576
Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
            180                 185                 190

GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG TAC TTC      624
Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
        195                 200                 205

AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC GTG      672
Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
    210                 215                 220

GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC GAG GCT      720
Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
225                 230                 235                 240

GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG CCA      768
Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
                245                 250                 255

GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT GCC      816
Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala
            260                 265                 270

GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT CTT      864
Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu
        275                 280                 285

CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA TTC      912
Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe
    290                 295                 300

CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG GAC      960
Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp
305                 310                 315                 320

TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG CTG     1008
Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu
                325                 330                 335

TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA AGT     1056
Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser
            340                 345                 350
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Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu
370 375 380

GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC GCC 1200
Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala
385 390 395 400

CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA TAT 1248
Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr
405 410 415

GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG AAC 1296
Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn
420 425 430

TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT AGA 1344
Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg
435 440 445

CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC ACT 1392
Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr
450 455 460

AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC GCC 1440
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala
465 470 475 480

GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC TTC AAC 1488
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn
485 490 495

CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC 1536
Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala
500 505 510

CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT GGC GAC 1584
Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp
515 520 525

GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAC GAG AGA TAC TAC 1632
Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr
530 535 540

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GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA GAC GTT     1680
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545                 550                 555                 560

GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT AAC     1728
Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn
                565                 570                 575

AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG CTG CTG     1776
Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu
            580                 585                 590

TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC TGC CAT     1824
Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His
        595                 600                 605

CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT AAG GTG     1872
Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val
    610                 615                 620

GAA CGC CTG AAA CAG GTG TTG CTC CAC CAA CAG GCT AAA TTT GGG AGA     1920
Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg
625                 630                 635                 640

AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA ACC     1968
Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr
                645                 650                 655

AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC CAT     2016
Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His
            660                 665                 670

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Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly
        675                 680                 685

ATT ACT AAT CTG AAA AAG TGC TCA ACC TCC CCC TCC TGG AAG CCT GTG     2112
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    690                 695                 700

AAT TC                                                              2117
Asn
705
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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             20                  25                  30

Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg
         35                  40                  45

Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
     50                  55                  60

Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
 65                  70                  75                  80

Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
                 85                  90                  95

Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
            100                 105                 110

Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
        115                 120                 125

Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
    130                 135                 140

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
145                 150                 155                 160

Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
                165                 170                 175

Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
            180                 185                 190

Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
        195                 200                 205
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Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
210 215 220

Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
225 230 235 240

Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
245 250 255

Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala
260 265 270

Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu
275 280 285

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290 295 300

Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp
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Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu
325 330 335

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340 345 350

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355 360 365

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370 375 380

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385 390 395 400

Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr
405 410 415

Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn
420 425 430

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435 440 445

Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr
450 455 460

Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala
465 470 475 480

Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn
485 490 495

Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala
500 505 510

Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp
515 520 525

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530 535 540

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545 550 555 560

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565 570 575

Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu
580 585 590

Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His
595 600 605

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610 615 620

Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg
625 630 635 640

Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr
645 650 655

Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His
660 665 670

Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly
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Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Ser Trp Lys Pro Val
690 695 700

Asn
705

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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TGT CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC        96
Cys Leu Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser
             20                  25                  30

CAA CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA       144
Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys
         35                  40                  45

GTG CGT GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG       192
Val Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln
     50                  55                  60

TGT ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT       240
Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp
 65                  70                  75                  80

GGT GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT       288
Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro
                 85                  90                  95

GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT       336
Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr
            100                 105                 110
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TAT GCC GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA 384

Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu
115 120 125

CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA 432

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130 135 140

TGG AAT GTC CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT 480

Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly
145 150 155 160

CCA CCT GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC 528

Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser
165 170 175

TGT GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG 576

Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu
180 185 190

TGT GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG 624

Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro
195 200 205

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Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly
210 215 220

GAC GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC 720

Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp
225 230 235 240

GAG GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG 768

Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg
245 250 255

AAG CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT 816

Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser
260 265 270

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CAT GCC GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG      864
His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp
        275                 280                 285

AAT CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG      912
Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro
    290                 295                 300

AAA TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC      960
Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe
305                 310                 315                 320

AAG GAC TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT     1008
Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser
                325                 330                 335

GGG CTG TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG     1056
Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg
            340                 345                 350

AAA AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT     1104
Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys
        355                 360                 365

GCG GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG     1152
Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu
    370                 375                 380

AGC GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC     1200
Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys
385                 390                 395                 400

ATC GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA     1248
Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly
                405                 410                 415

GGA TAT GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA     1296
Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala
            420                 425                 430
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GAG AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG 1344

Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val
435 440 445

GAT AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA 1392

Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser
450 455 460

GAC ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC 1440

Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His
465 470 475 480

ACC GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC 1488

Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu
485 490 495

TTC AAC CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC 1536

Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser
500 505 510

TGT GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT 1584

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515 520 525

GGC GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAC GAG AGA 1632

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530 535 540

TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA 1680

Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly
545 550 555 560

GAC GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA 1728

Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly
565 570 575

AAT AAC AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG 1776

Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala
580 585 590

```
CTG CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC     1824
Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser
        595                 600                 605

TGC CAT CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT     1872
Cys His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp
    610                 615                 620

AAG GTG GAA CGC CTG AAA CAG GTG TTG CTC CAC CAA CAG GCT AAA TTT     1920
Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe
625                 630                 635                 640

GGG AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT     1968
Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser
                645                 650                 655

GAA ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA     2016
Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg
            660                 665                 670

CTC CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC     2064
Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val
        675                 680                 685

GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA     2112
Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu
    690                 695                 700

GCC TGT GAA TTC                                                     2124
Ala Cys Glu Phe
705
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Lys Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu
1               5                   10                  15

Cys Leu Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser
            20                  25                  30

Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys
        35                  40                  45

Val Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln
    50                  55                  60

Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp
65                  70                  75                  80

Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro
                85                  90                  95

Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr
            100                 105                 110

Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu
        115                 120                 125

Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly
    130                 135                 140

Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly
145                 150                 155                 160

Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser
                165                 170                 175

Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu
            180                 185                 190

Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro
        195                 200                 205
```

Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly
210 215 220

Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp
225 230 235 240

Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg
245 250 255

Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser
260 265 270

His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp
275 280 285

Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro
290 295 300

Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe
305 310 315 320

Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser
325 330 335

Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg
340 345 350

Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys
355 360 365

Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu
370 375 380

Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys
385 390 395 400

Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly
405 410 415

Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala
420 425 430

Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val
435 440 445

Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser
450 455 460

Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His
465 470 475 480

```
Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu
                485                 490                 495

Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser
            500                 505                 510

Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile
        515                 520                 525

Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg
    530                 535                 540

Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly
545                 550                 555                 560

Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly
                565                 570                 575

Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala
            580                 585                 590

Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser
        595                 600                 605

Cys His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp
    610                 615                 620

Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe
625                 630                 635                 640

Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser
                645                 650                 655

Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg
            660                 665                 670

Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val
        675                 680                 685

Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu
    690                 695                 700

Ala Cys Glu Phe
705
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAGGATCAT GGCTCACTGC CACCTTCATC TCCCAGGCTC AAATGGTCCT CCCACTTTAG 60

CCTCCCAAGT AGCTGGGACC ATAGGCATAC ACCACCATGC TGGGCTAATT TTTGTATTTT 120

TTGTAGAGAT GGGGGTTTCC CTATGAAGCC CAGGCTAGTC TTGAACTCCT GGGCTCAAGC 180

GATCCTCCCA TCTTGGCCTC CCAAAGTGCT GGGATTACAG GCATGAGCCA CTGTGCCCTG 240

CCTAGTTACT CTTGGGCTAA GTTCACATCC ATACACACAG GATATTCTTT CTGAGGCCCC 300

CAATGTGTCC CACAGGCACC ATGCTGTATG TGACACTCCC CTAGAGATGG ATGTTTAGTT 360

TGCTTCCAAC TGATTAATGG CATGCAGTGG TGCCTGGAAA CATTTGTACC TGGGGTGCTG 420

TGTGTCATGG GAATGTATTT ACGAGATGTA TTCTTAGAAG CAGTATTCTA GCTTTTGAAT 480

TTTAAAATCT GACATTTATG GCGATTGTTA AAATGAGGTT ACCATTTCCT ACTGAATACT 540

ATCAACACCA AAAAAGAAGA AGGAGGAGAT GGAGAAAAAA AAGACAAAAA AAAAAAAAGT 600

GGTAGGGCAT CTTAGCCATA GGGCATCTTT CTCATTGGCA AATAAGAACA TGGAACCAGC 660

CTTGGGTGGT GGCCATTCCC CTCTGAGGTC CCTGTCTGTT TTCTGGGAGC TGTATTGTGG 720

GTCTCAGCAG GGCAGGGAGA TACCCCATGG GCAGCTTGCC TGAGACTCTG GGCAGCCTCT 780

CTTTTCTCTG TCAGCTGTCC CTAGGCTGCT GCTGGGGGTG GTCGGGTCAT CTTTTCAACT 840

CTCAGCTCAC TGCTGAGCCA AGGTGAAAGC AAACCCACCT GCCCTAACTG GCTCCTAGGC 900

ACCTTCAAGG TCATCTGCTG AAGAAGATAG CAGTCTCACA GGTCAAGGCG ATCTTCAAGT 960

AAAGACCCTC TGCTCTGTGT CCTGCCCTCT AGAAGGCACT GAGACCAGAG CTGGGACAGG 1020

GCTCAGGGGG CTGCGACTCC TAGGGGCTTG CAGACCTAGT GGGAGAGAAA GAACATCGCA 1080

GCAGCCAGGC AGAACCAGGA CAGGTGAGGT GCAGGCTGGC TTTCCTCTCG CAGCGCGGTG 1140

TGGAGTCCTG TCCTGCCTCA GGGCTTTTCG GAGCCTGGAT CCTCAAGGAA CAAGTAGACC 1200

TGGCCGCGGG GAGTGGGGAG GGAAGGGGTG TCTATTGGGC AACAGGGCGG GGCAAAGCCC 1260

TGAATAAAGG GGCGCAGGGC AGGCGCAAGT GGCAGAGCCT TCGTTTGCCA AGTCGCCTCC 1320

AGACCGCAGA CATGAAACTT GTCTTCCTCG TCCTGCTGTT CCTCGGGGCC CTCGGTGAGT 1380

GCAGGTGCCT GGGGGCGCGA GCCGCCTGAT GGGCGTCTCC TGCGCCCTGT CTGCTAGGCG 1440

CTTTGGTCCC TGTGTCCGGT TGGCTGGGCG CGGGGTCTCT GCGCCCCGCG GTCCCAGCGC 1500

CTACAGCCGG GAGGCGGCCC GGACGCGGGG CCAGTCTCTT TCCCACATGG GGAGGAACAG 1560

GAGCTGGGCT CCTCAAGCCG GATCGGGGCA CGCCTAGCTC TGCTCAGAGC TTCTCAAAAG 1620

GCCTCCCAGG CCCCTGTCCC TTTGTGTCCC GCCTAAGGAT TTGGTCCCCA TTGTATTGTG 1680

ACATGCGTTT TACCTGGGAG GAAAGTGAGG CTCAGAGAGG GTGAGCGACT AGCTCAAGGA 1740

CCCTAGTCCA GATCCTAGCT CCTGCGAGGA CTGTGAGACC CCAGCAAGAC CGAGCCTTTA 1800

TGAGACTTAG TTTCTTCACT TAAAGAAACG GCCTAACCAT GGGTCCACAG GGTTGTGAGG 1860

AGGAGATGGG GCATTCGCAC ACCTTCCGTG GCAGAGGGTT GTGGAGGGGT GCGGTGCTCC 1920

TGATGGAACC CTGTGTCAGA GGGTTTGAGA GGGAAATGTC AGCCAAACAG AAGGAAGGAG 1980

CAGAAGGAAG GAAACAATTG TCAGTTCCAT AACCAAAGTA ATTTCTCGGG TGCTCAGAGG 2040

GCACTCCCCA GCGCTGCACA TTAGTGACCT AAATGCGTGA GTGCGG 2086

WHAT IS CLAIMED IS:

1. A DNA segment encoding human lactoferrin according to sequence I.D. No.: 1.

2. Human lactoferrin protein according to sequence I.D. No.: 2.

3. A DNA promotor region for human lactoferrin according to sequence I.D. No.: 5 and allelic variations thereof.

4. A recombinant DNA construct comprising:
i) said DNA segment according to claim 1 and
ii) a vector

5. The DNA construct according to claim 4 further comprising the regulating sequence according to sequence I.D. No.: 5 or portion thereof operatively linked to said DNA fragment.

6. The DNA construct according to claim 4 or 5 wherein said vector is pAc 700 series.

7. A host cell comprising said DNA construct according to claim 4 or 5.

8. The cell according to claim 7, wherein said host cell is Sf9 cells.

9. A recombinant lactoferrin protein expressed in the host cell of claim 7.

10. A method of treating a condition in a patient characterization by a deficiency in

lactoferrin, administering to said patient an amount of human lactoferrin according to claims 2 or 9 sufficient to eliminate said deficiency.

11. The method of claim 10 wherein said condition is neutropenia, AIDS, skin infection, gastrointestinal bacterial overgrowth syndrome, vaginal infection or septic shock.

12. A method of diagnosing malignancy in a biological sample comprising the steps of:
    i) isolating DNA from said biological sample and normal control sample
    ii) cutting said DNA with restriction enzyme, Xba I,
    iii) hybridizing said cut DNA of step (ii) with a DNA segment according to claim 1 or 2 or portion thereof under conditions such that hybridization is effected and
    iv) comparing the hybridization products of step 3 from said biological sample and normal sample to each other.

13. A method of detecting recovery of a disease in a patient given a therapeutic comprising the steps of:
    i) isolating DNA from a biological sample of said patient and normal human control sample,
    ii) cutting said DNA with Xba I,
    iii) hybridizing said cut DNA of step (ii) with a DNA segment according to claim 1 or

portion thereof under conditions such that hybridization is effected and

iv) comparing the hybridization products of the biological sample in step 3 to the hybridization products of normal sample in step 3 to determine the relatedness to normal samples.

14. A method for detecting insertions, deletions or mutations surrounding the human lactoferrin gene comprising the steps of

i) isolating DNA from a biological sample suspected of having said insertion, deletion or mutation,

ii) amplifying said DNA using the DNA fragment of claim 1 or portion thereof in a polymerase chain reaction,

iii) cuting said amplified DNA with restriction enzyme Xbu I,

iv) hybridizing said DNA from steo (iii) with the DNA fragment according to claim 1 or portion thereof under condistions such that hybridization is effected and

v) sequencing said DNA of step (iv).

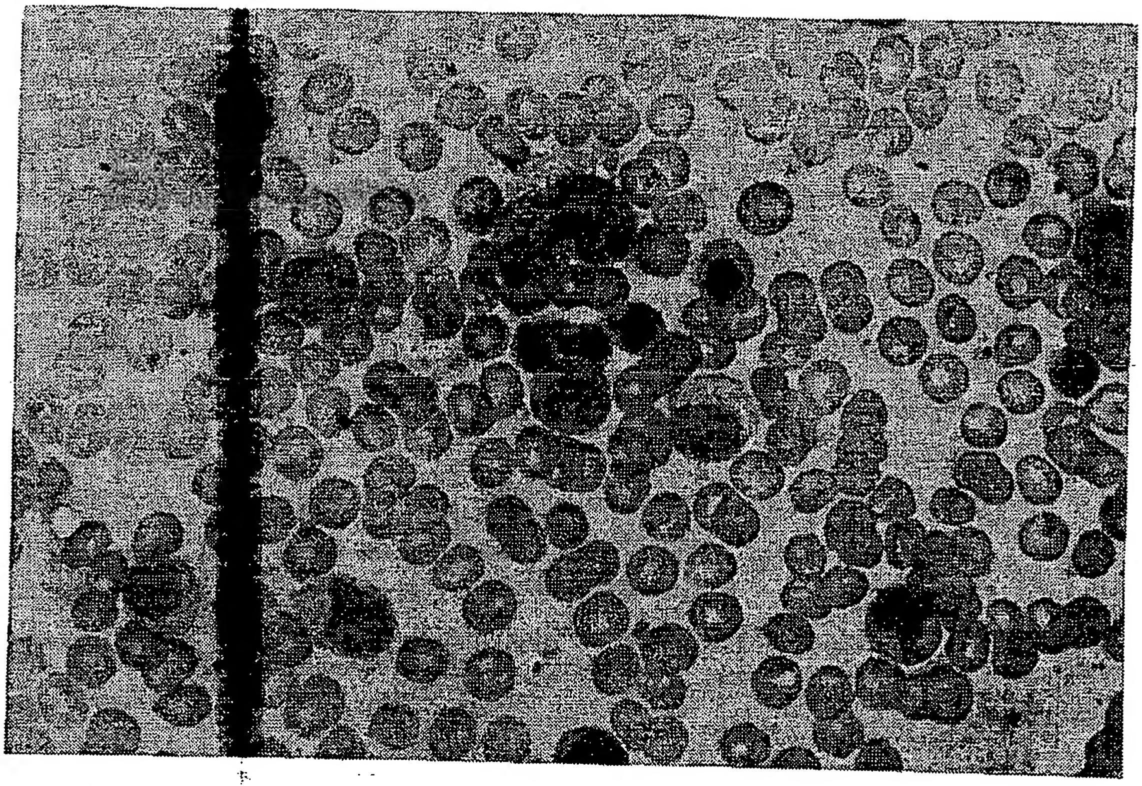


FIG. 1A

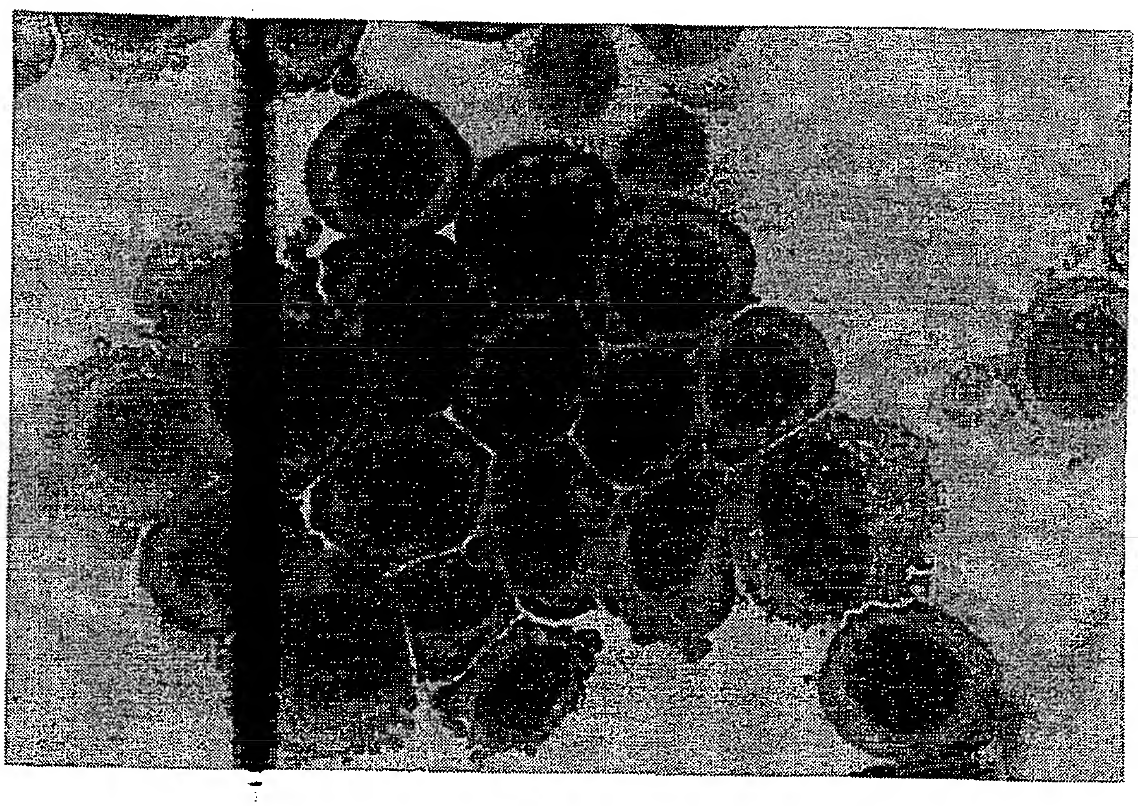


FIG. 1B

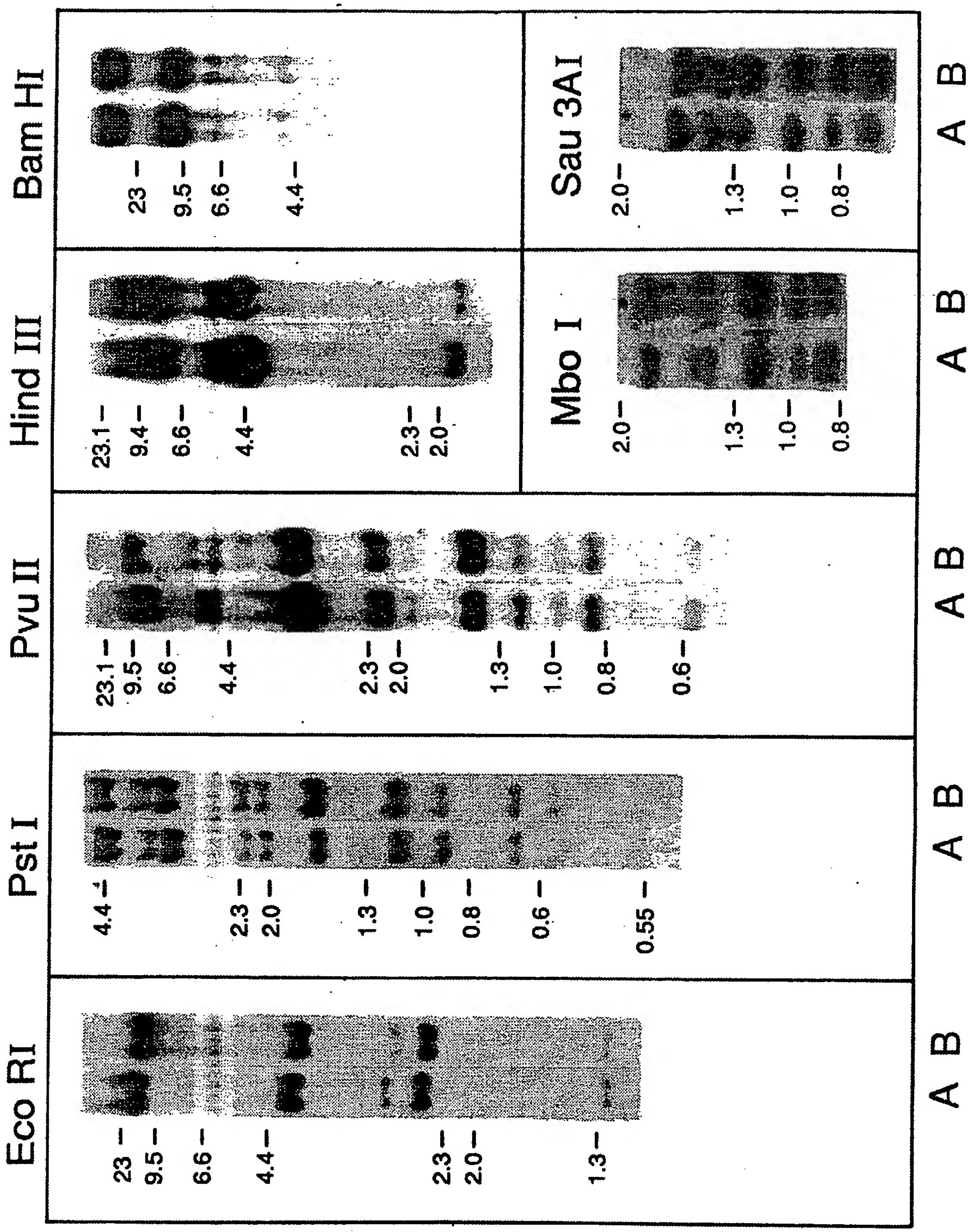

Bam HI
23
9.5
6.6
4.4
Hind III
23.1
9.4
6.6
4.4
2.3
2.0
Sau 3AI
2.0
1.3
1.0
0.8
Mbo I
2.0
1.3
1.0
0.8
Pvu II
23.1
9.5
6.6
4.4
2.3
2.0
1.3
1.0
0.8
0.6
Pst I
4.4
2.3
2.0
1.3
1.0
0.8
0.6
0.55
Eco RI
23
9.5
6.6
4.4
2.3
2.0
1.3
A B
A B
A B
A B
A B
A B

FIG. 2

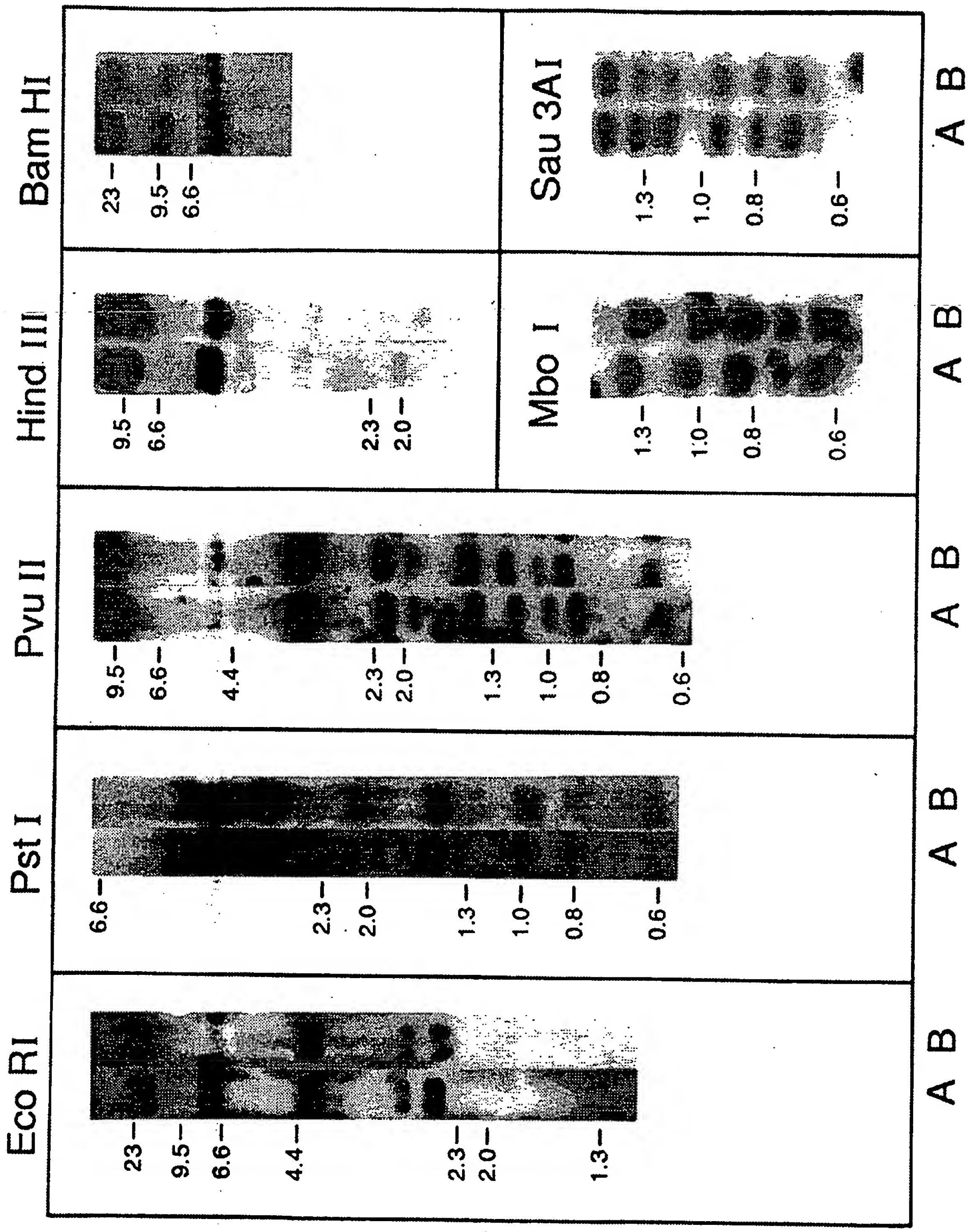

Bam HI
23
9.5
6.6
Hind III
9.5
6.6
2.3
2.0
Pvu II
9.5
6.6
4.4
2.3
2.0
1.3
1.0
0.8
0.6
Pst I
6.6
2.3
2.0
1.3
1.0
0.8
0.6
Eco RI
23
9.5
6.6
4.4
2.3
2.0
1.3
Sau 3AI
1.3
1.0
0.8
0.6
Mbo I
1.3
1.0
0.8
0.6
A B
A B
A B
A B
A B

FIG. 3

FIG. 4

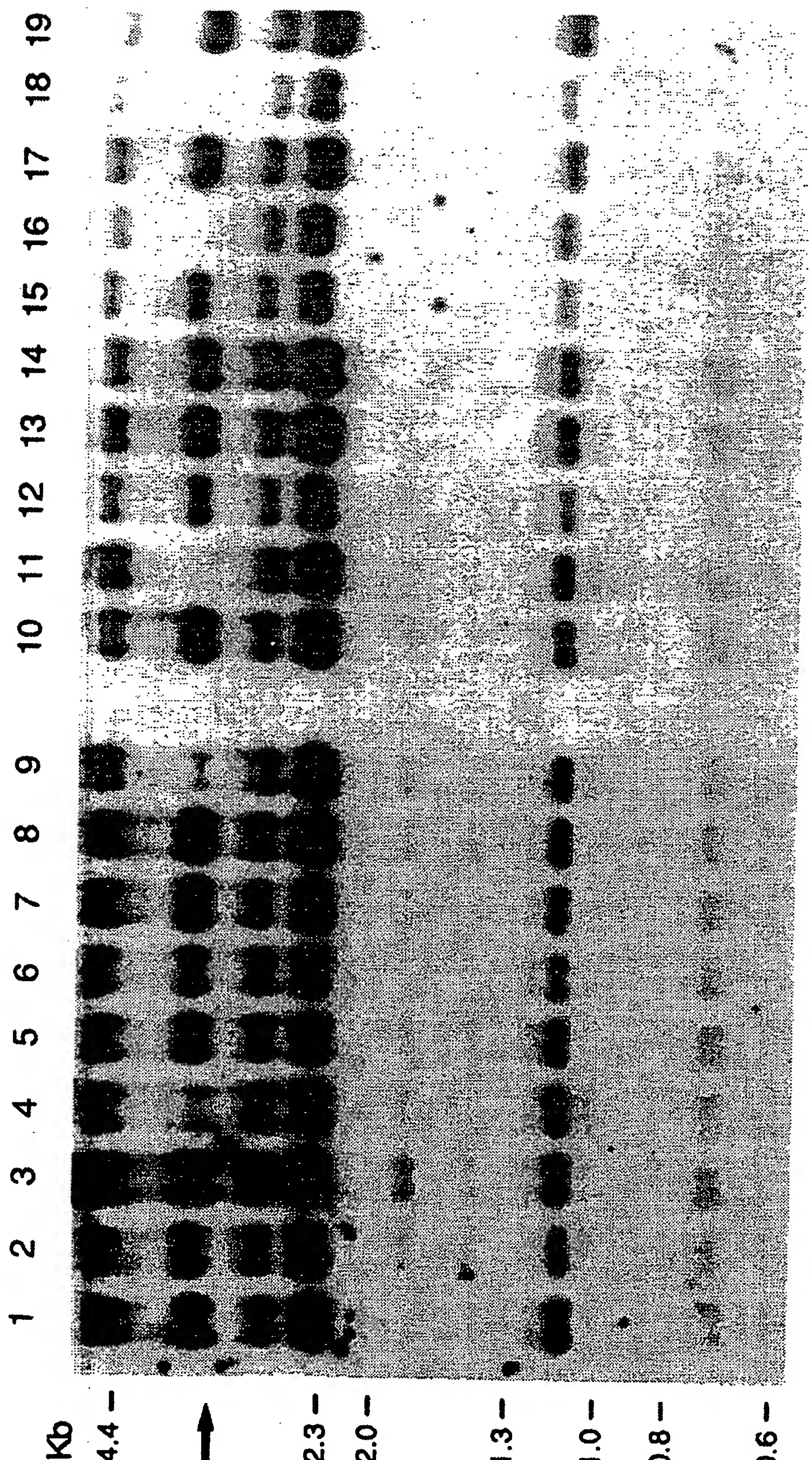
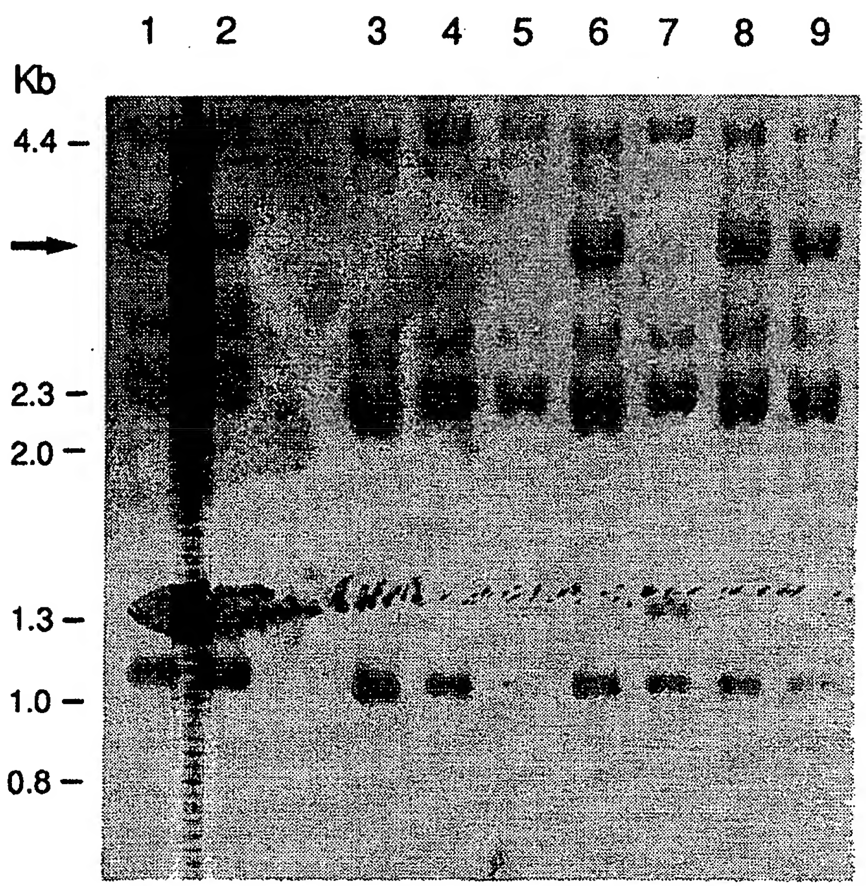


FIG. 5



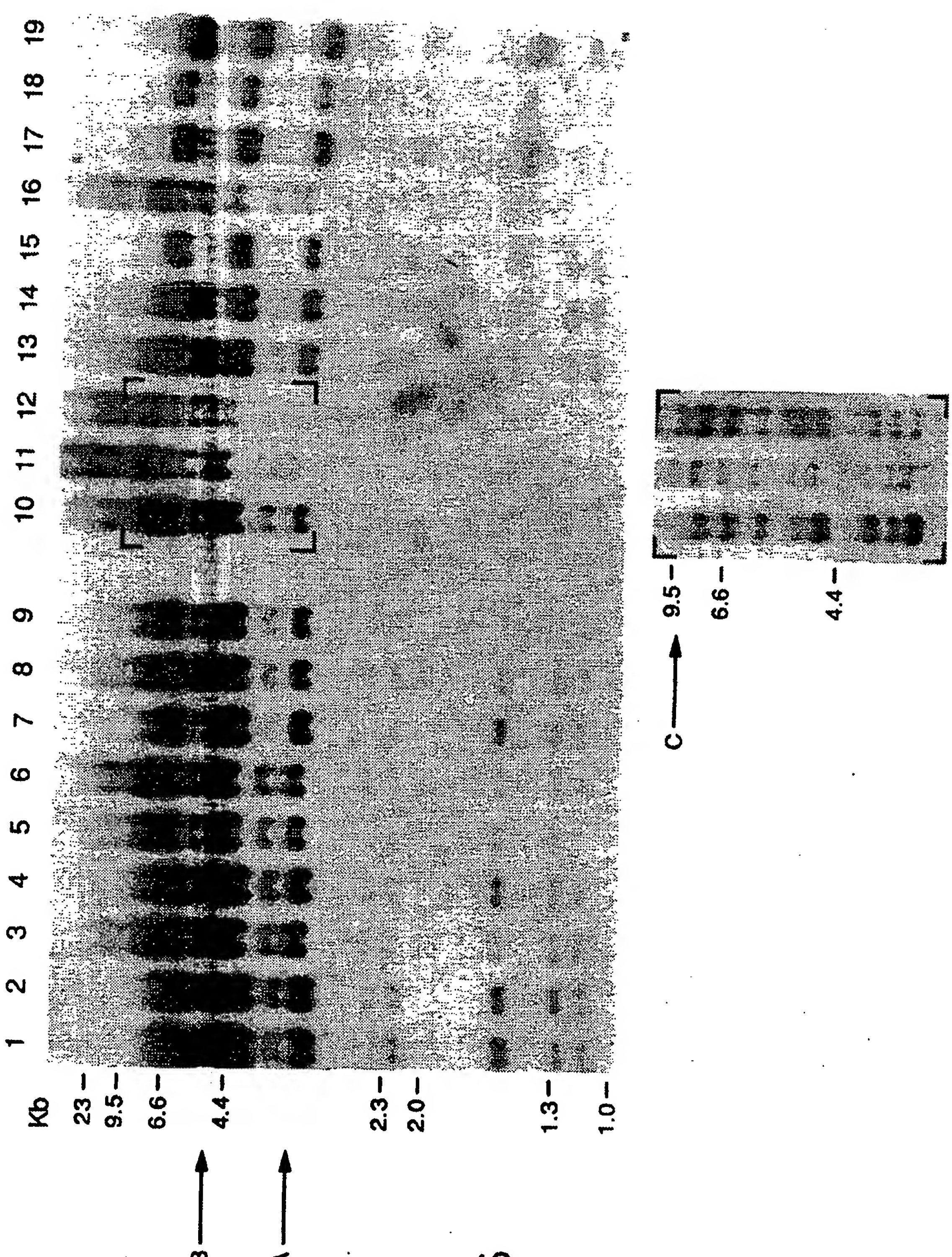

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
Kb
23
9.5
6.6
4.4
2.3
2.0
1.3
1.0
B
A
C
9.5
6.6
4.4

FIG. 6

FIG. 7

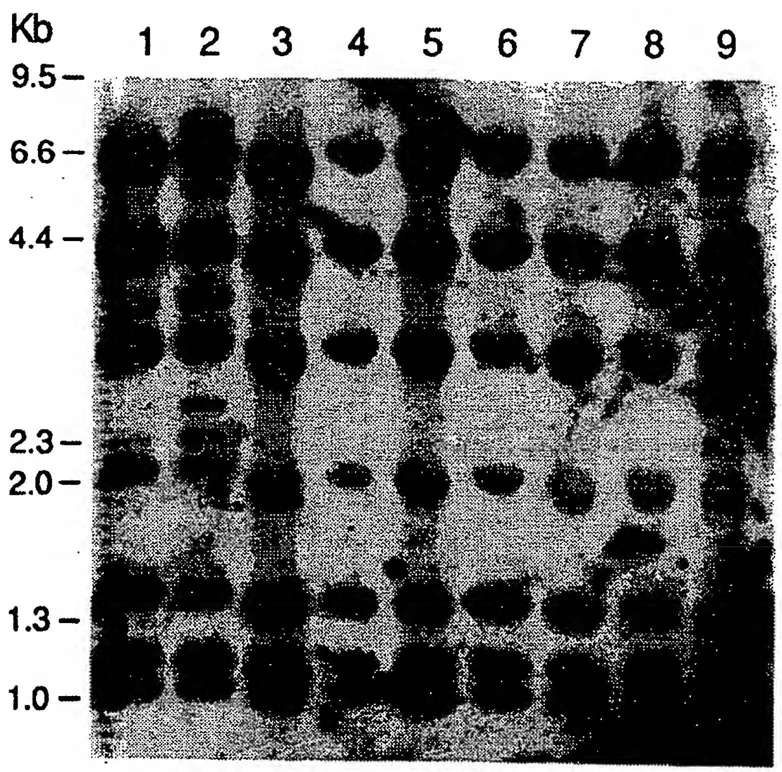
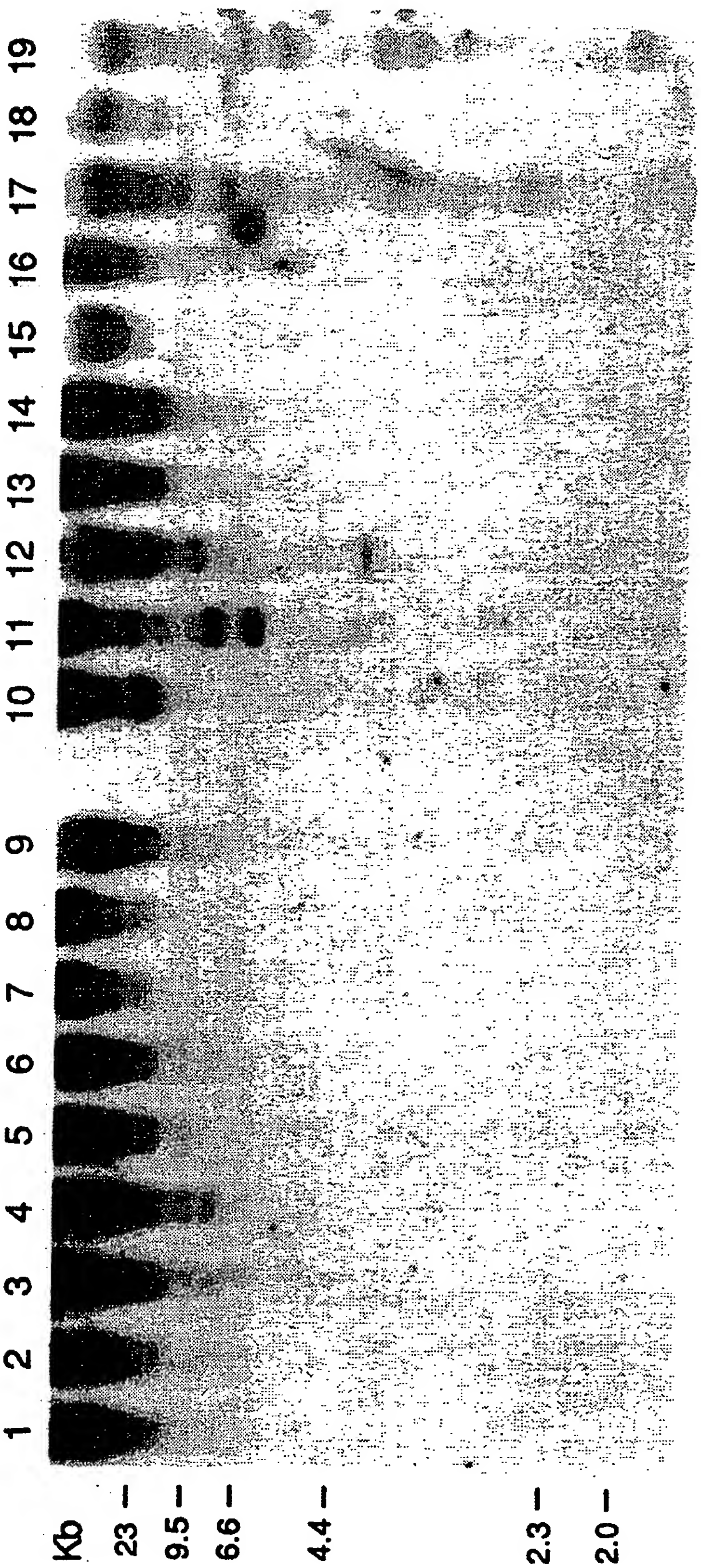


FIG. 8



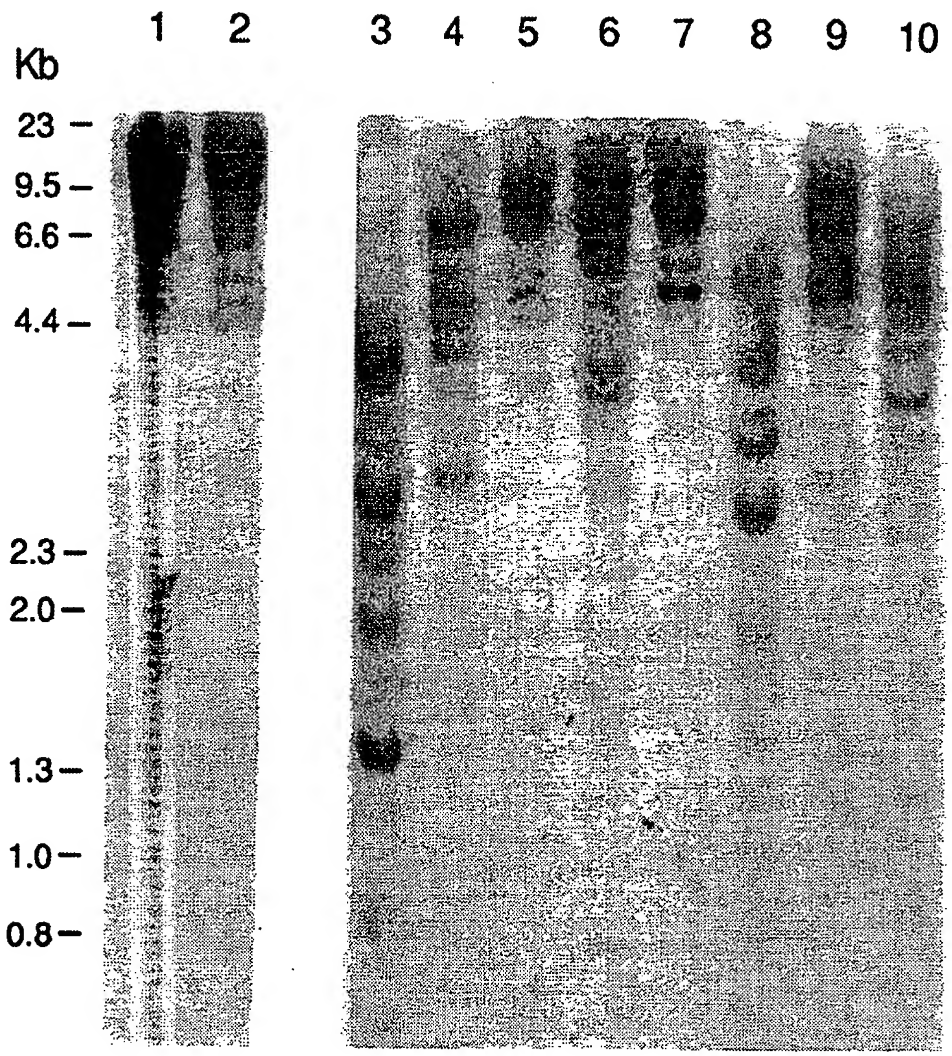


FIG. 9

FIG. 10A

1	CTT	GTC	TTC	CTC	GTC	CTG	CTG	TTC	CTC	GGG	GCC	CTC	GGA	CTG	TGT	CTG
	Leu	Val	Phe	Leu	Val	Leu	Leu	Phe	Leu	Gly	Ala	Leu	Gly	Leu	Cys	Leu
	GCT	GGC	CGT	AGG												
	Ala	Gly	Arg	Arg												
61	AGA	AGG	AGT	GTT	CAG	TGG	TGC	GCC	GTA	TCC	CAA	CCC	GAG	GCC	ACA	AAA
	Arg	<u>Arg</u>	Ser	Val	Gln	Trp	Cys	Ala	Val	Ser	Gln	Pro	Glu	Ala	Thr	Lys
											Asn					
	TGC	TTC	CAA	TGG												
	Cys	Phe	Gln	Trp												
121	CAA	AGG	AAT	ATG	AGA	AAA	GTG	CGT	GGC	CCT	CCT	GTC	AGC	TGC	ATA	AAG
	Gln	Arg	Asn	Met	Arg	Lys	Val	Arg	Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys
															Leu	
	AGA	GAC	TCC	CCC												
	Arg	Asp	Ser	Pro												
181	ATC	CAG	TGT	ATC	CAG	GCC	ATT	GCG	GAA	AAC	AGG	GCC	GAT	GCT	GTG	ACC
	Ile	Gln	Cys	Ile	Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr
	CTT	GAT	GGT	GGT												
	Leu	Asp	Gly	Gly												

FIG. 10B

```
241  TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT GTA GCG
     Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala

     GCG GAA GTC TAC
     Ala Glu Val Tyr

301  GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT GCC GTG GCT GTG GTG
     Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val Ala Val Val

     AAG AAG GGC GGC
     Lys Lys Gly Gly

361  AGC TTT CAG CTG AAC GAA CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC
     Ser Phe Gln Leu Asn Glu Leu Gln Gly Leu Lys Ser Cys His Thr Gly

     CTT CGC AGG ACC
     Leu Arg Arg Thr

                                  C
421  GCT GGA TGG AAT GTC CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG
     Ala Gly Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp
                             Thr

     ACG GGT CCA CCT
     Thr Gly Pro Pro
```

FIG. 10C

```
481  GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC TGT GTT
     Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val

     CCC GGT GCA GAT
     Pro Gly Ala Asp

541  AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT GCG GGG ACA GGG GAA
     Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly Thr Gly Glu

     AAC AAA TGT GCC
     Asn Lys Cys Ala

601  TTC TCC TCC CAG GAA CCG TAC TTC AGC TAC TCT GGT GCC TTC AAG TGT
     Phe Ser Ser Gln Glu Pro Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys

     CTG AGA GAC GGG
     Leu Arg Asp Gly
         Lys

661  GCT GGA GAC GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG
     Ala Gly Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu

     TCA GAC GAG GCT
     Ser Asp Glu Ala
```

FIG. 10D

```
721  GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG CCA
     Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro

     GTG GAC AAG TTC
     Val Asp Lys Phe

781  AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT GCC GTT GTG GCA CGA
     Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val Val Ala Arg

     AGT GTG AAT GGC
     Ser Val Asn Gly

841  AAG GAG GAT GCC ATC TGG AAT CTT CTC CGC CAG GCA CAG GAA AAG TTT
     Lys Glu Asp Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe

     GGA AAG GAC AAG
     Gly Lys Asp Lys

901  TCA CCG AAA TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG
     Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu

     CTG TTC AAG GAC
     Leu Phe Lys Asp
```

FIG. 10E

```
961   TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG CTG
      Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu

      TAC CTT GGC TCC
      Tyr Leu Gly Ser

1021  GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA AGT GAG GAG GAA GTG
      Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu Glu Glu Val

      GCT GCC CGG CGT
      Ala Ala Arg Arg

1081  GCG CGG GTC GTG TGG TGT GCG GTG GGC GAG CAG GAG CTG CGC AAG TGT
      Ala Arg Val Val Trp Cys Ala Val Gly Glu Gln Glu Leu Arg Lys Cys

      AAC CAG TGG AGT
      Asn Gln Trp Ser

1141  GGC TTG AGC GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG
      Gly Leu Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu

      TAC CTT GGC TCC
      Tyr Leu Gly Ser
```

FIG. 10F

```
1201   CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA TAT
       Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr

       GTG TAC ACT GCA
       Val Tyr Thr Ala

       T
1261   GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG AAC TAC AAA TCC CAA
       Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Lys Ser Gln
       Cys

       CAA AGC AGT GAC
       Gln Ser Ser Asp

1321   CCT GAT CCT AAC TGT GTG GAT AGA CCT GTG GAA GGA TAT CTT GCT GTG
       Pro Asp Pro Asn Cys Val Asp Arg Pro Val Glu Gly Tyr Leu Ala Val

       GCG GTG GTT AGG
       Ala Val Val Arg

1381   AGA TCA GAC ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC
       Arg Ser Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser

       TGC CAC ACC GCC
       Cys His Thr Ala
```

FIG. 10G

```
                            GC
1441  GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC TTC AAC
      Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn
                          Ala

      CAG ACG GGC TCC
      Gln Thr Gly Ser

1501  TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC CCT GGG TCT GAC
      Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro Gly Ser Asp

      CCG AGA TCT AAT
      Pro Arg Ser Asn

1561  CTC TGT GCT CTG TGT ATT GGC GAC GAG CAG GGT GAG AAT AAG TGC GTG
      Leu Cys Ala Leu Cys Ile Gly Asp Glu Gln Gly Glu Asn Lys Cys Val

                    T
      CCC AAC AGC AAC
      Pro Asn Ser Asn

1621  GAG AGA TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT
      Glu Arg Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn

      GCT GGA GAC GTT
      Ala Gly Asp Val
```

FIG. 10H

```
1681  GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT AAC
      Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn

      AAT GAG GCA TGG
      Asn Glu Ala Trp

1741  GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG CTG CTG TGC CTC GAT GGC
      Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys Leu Asp Gly

      AAA CGG AAG CCT
      Lys Arg Lys Pro

1801  GTG ACT GAG GCT AGA AGC TGC CAT CTT GCC ATG GCC CCG AAT CAT GCC
      Val Thr Glu Ala Arg Ser Cys His Leu Ala Met Ala Pro Asn His Ala

      GTG GTG TCT CGG
      Val Val Ser Arg

                                                C
1861  ATG GAT AAG GTG GAA CGC CTG AAA CAG GTG TTG CTC CAC CAA CAG GCT
      Met Asp Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala

      AAA TTT GGG AGA
      Lys Phe Gly Arg
```

FIG. 10I

```
1921  AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA ACC
      Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr

      AAA AAC CTT CTG
      Lys Asn Leu Leu

1981  TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC CAT GGC AAA ACA ACA
      Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly Lys Thr Thr

      TAT GAA AAA TAT
      Tyr Glu Lys Tyr

2041  TTG GGA CCA CAG TAT GTC GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA
      Leu Gly Pro Gln Tyr Val Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser

                  C
      ACC TCC CCC TCC
      Thr Ser Pro Ser
                  Leu

2101  TGG AAG CCT GTG AAT TC 2117
      Trp Lys Pro Val Asn
      Leu Glu Ala Cys Glu Phe
```

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/04012

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :C12N 15/00, 15/10, 15/12; A61K 35/20
US CL :435/6, 69.1, 320.1; 514/6; 530/395, 400; 536/27
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 69.1, 69.6, 320.1; 514/6; 530/350, 395, 400; 536/27

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, BIOSIS, World Patents Index
search terms: lactoferrin, gene, DNA, cDNA, breast cancer, cancer

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	Clinica Chimica Acta, Vol. 151, issued 1985, W.R. Bezwoda et al, "Enzyme linked immunosorbent assay for lactoferrin. Plasma and tissue measurements", pages 61-69, entire document.	2,9 1,3-8,10-11
X Y	Clinica Chimica Acta, Vol. 157, issued 1986, W.R. Bezwoda et al, "Isolation and characterisation of lactoferrin separate from human whey by adsorption chromatography using Cibacron Blue F3G-A linked affinity adsorbent", pages 89-94, entire document.	2,9 1,3-8
X Y	FEBS Letters, Vol. 109, no. 2, issued January 1980, L. Blackberg et al, "Isolation of lactoferrin from human whey by a single chromatographic step", pages 180-184, entire document.	2,9 1,3-8
Y	J. Sambrook et al., "Molecular cloning techniques, a laboratory manuel", published 1989 by Cold Spring Harbor Laboratory Press, pages 12.2-12.15, entire document.	1,3-8

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be part of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 July 1992	31 JUL 1992
Name and mailing address of the ISA/ Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. NOT APPLICABLE	Authorized officer DIAN COOK Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)★

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/04012

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Cancer Research, Vol. 46, no. 3, issued March 1986, K. Shirasuna et al, "Isolation and characterization of different clones including myoepithelial-like variants from a clonal neoplastic epithelial duct cell line of human salivary gland origin", pages 1418-1426, especially abstract.	12-14